

SEQUENCE LISTING

<110> He, et al.

<120> Interleukin-1 Beta Converting Enzyme Like Apoptosis Protease 3  
and 4

<130> PF140P1D2

<140> To Be Assigned

<141> 2004-03-17

<150> 09/613,508

<151> 2000-07-10

<150> 08/462,969

<151> 1995-06-05

<150> 08/334,251

<151> 1994-11-01

<160> 14

<170> PatentIn version 3.2

<210> 1

<211> 1369

<212> DNA

<213> Homo sapiens

<400> 1

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gcggggacac gggtcgcttt gggctttcc acccctgcgg agcgcactac cccgagccag	180
ggcgggtgca agccccgccc ggccttaccc agggcggttc ctccctccgc agcgccgaga	240
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actgtgccag tcccagccgc cttaccgcgg tgggaacgtt ggcagatgtt cagggctgtt	360
ttgaagagca gggggtttagt gattcagcaa atgaagattc agtggatgtt aagccagacc	420
ggtcctcggtt tgtaccgtcc ctcttcagta agaagaagaa aaatgtcacc atgcgtatcca	480
tcaagaccac ccgggaccga gtgcctacat atcagtacaa catgaatttt gaaaagctgg	540
gcaaataatgcataataaaac aacaagaact ttgataaaagt gacaggtatg ggcttcgaa	600
acggaacaga caaagatgcc gaggcgctct tcaagtgcctt ccgaagcctg ggttttgacg	660
tgattgtcta taatgactgc tcttgccca agatgcaaga tctgcttaaa aaagcttctg	720
aagaggacca tacaaatgcc gcctgcttcg cctgcattcct cttaagccat ggagaagaaa	780
atgtatattt tggaaagat ggtgtcacac caataaagga tttgacagcc cacttttaggg	840
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gctattactc	gtggaggagc	ccaggaagag	gctcctggtt	tgtgcaagcc	ctctgctcca	1080
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ggtacattct	agctgagaag	caatgggtca	ctcattaatg	aatcacattt	ttttatgctc	1320
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<210> 2  
<211> 303  
<212> PRT  
<213> Homo sapiens

<400> 2

Met	Ala	Asp	Asp	Gln	Gly	Cys	Ile	Glu	Glu	Gln	Gly	Val	Glu	Asp	Ser
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Ala	Asn	Glu	Asp	Ser	Val	Asp	Ala	Lys	Pro	Asp	Arg	Ser	Ser	Phe	Val
				20				25					30		

Pro	Ser	Leu	Phe	Ser	Lys	Lys	Lys	Asn	Val	Thr	Met	Arg	Ser	Ile
					35		40				45			

Lys	Thr	Thr	Arg	Asp	Arg	Val	Pro	Thr	Tyr	Gln	Tyr	Asn	Met	Asn	Phe
						50		55			60				

Glu	Lys	Leu	Gly	Lys	Cys	Ile	Ile	Ile	Asn	Asn	Lys	Asn	Phe	Asp	Lys
	65					70			75				80		

Val	Thr	Gly	Met	Gly	Val	Arg	Asn	Gly	Thr	Asp	Lys	Asp	Ala	Glu	Ala
			85					90					95		

Leu	Phe	Lys	Cys	Phe	Arg	Ser	Leu	Gly	Phe	Asp	Val	Ile	Val	Tyr	Asn
					100			105				110			

Asp	Cys	Ser	Cys	Ala	Lys	Met	Gln	Asp	Leu	Leu	Lys	Lys	Ala	Ser	Glu
					115			120				125			

Glu	Asp	His	Thr	Asn	Ala	Ala	Cys	Phe	Ala	Cys	Ile	Leu	Leu	Ser	His
						130		135				140			

Gly Glu Glu Asn Val Ile Tyr Gly Lys Asp Gly Val Thr Pro Ile Lys  
145 150 155 160

Asp Leu Thr Ala His Phe Arg Gly Asp Arg Cys Lys Thr Leu Leu Glu  
165 170 175

Lys Pro Lys Leu Phe Phe Ile Gln Ala Cys Arg Gly Thr Glu Leu Asp  
180 185 190

Asp Ala Ile Gln Ala Asp Ser Gly Pro Ile Asn Asp Thr Asp Ala Asn  
195 200 205

Pro Arg Tyr Lys Ile Pro Val Glu Ala Asp Phe Leu Phe Ala Tyr Ser  
210 215 220

Thr Val Pro Gly Tyr Tyr Ser Trp Arg Ser Pro Gly Arg Gly Ser Trp  
225 230 235 240

Phe Val Gln Ala Leu Cys Ser Ile Leu Glu Glu His Gly Lys Asp Leu  
245 250 255

Glu Ile Met Gln Ile Leu Thr Arg Val Asn Asp Arg Val Ala Arg His  
260 265 270

Phe Glu Ser Gln Ser Asp Asp Pro His Phe His Glu Lys Lys Gln Ile  
275 280 285

Pro Cys Val Val Ser Met Leu Thr Lys Glu Leu Tyr Phe Ser Gln  
290 295 300

<210> 3

<211> 1159

<212> DNA

<213> Homo sapiens

<400> 3

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gccgtgagga gttagcgagc cctgctcaca ctcggcgctc tggtttcgg tgggtgtgcc 180

ctgcacacctgc ctcttccccgc attctcatta ataaaggatccat ccatggagaa cactgaaaac 240

tcagtggatt caaaatccat taaaaatttg gaaccaaaga tcatacatgg aagcgaatca 300

atggactctg gaatatccct ggacaacagt tataaaatgg attatcctga gatgggttta 360

tgtataataa ttaataataa gaattttcat aaaagcactg gaatgacatc tcgggtctgg 420

acagatgtcg atgcagcaaa cctcagggaa acattcagaa acttcaaata tgaagtcaagg	480
aataaaaatg atcttacacg tgaagaatttga tgcgtatgt ttctaaagaa	540
gatcacagca aaaggagcag ttttgggtgt gtgcctctga gccatggta agaaggaata	600
attttggaa caaatggacc tggtgacctg aaaaaaataa caaactttt cagagggat	660
cgtttagaa gtctaactgg aaaacccaaa cttttcatta ttcaggcctg ccgtggtaca	720
gaactggact gtggcattga gacagacagt ggtgttcatg atgacatggc gtgtcataaa	780
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cgaaattcaa aggatggctc ctgggtcattc cagtcgctt gtgccatgct gaaacagtat	900
gccgacaagc ttgaatttat gcacattctt acccgggtta accgaaaggt ggcaacagaa	960
tttgagtccct tttcctttga cgctactttt catgcaaaga aacagattcc atgtattgtt	1020
tccatgctca caaaagaact ctattttat cactaaagaa atggttgggt ggtggtttt	1080
tttagtttgt atgccaagtg agaagatggt atattgggt actgtatttc cctctcattg	1140
gggacctact ctcatgctg	1159

<210> 4  
 <211> 277  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Met Glu Asn Thr Glu Asn Ser Val Asp Ser Lys Ser Ile Lys Asn Leu			
1	5	10	15

Glu Pro Lys Ile Ile His Gly Ser Glu Ser Met Asp Ser Gly Ile Ser			
20	25	30	

Leu Asp Asn Ser Tyr Lys Met Asp Tyr Pro Glu Met Gly Leu Cys Ile			
35	40	45	

Ile Ile Asn Asn Lys Asn Phe His Lys Ser Thr Gly Met Thr Ser Arg			
50	55	60	

Ser Gly Thr Asp Val Asp Ala Ala Asn Leu Arg Glu Thr Phe Arg Asn			
65	70	75	80

Leu Lys Tyr Glu Val Arg Asn Lys Asn Asp Leu Thr Arg Glu Glu Ile			
85	90	95	

Val Glu Leu Met Arg Asp Val Ser Lys Glu Asp His Ser Lys Arg Ser	
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100

105

110

Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe  
115 120 125

Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg  
130 135 140

Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile  
145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser  
165 170 175

Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Glu Ala Asp  
180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn  
195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys  
210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn  
225 230 235 240

Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe  
245 250 255

His Ala Lys Lys Gln Ile Pro Cys Ile Val Ser Met Leu Thr Lys Glu  
260 265 270

Leu Tyr Phe Tyr His  
275

<210> 5

<211> 31

<212> DNA

<213> Artificial sequence

<220>

<223> Contains a Bam HI restriction enzyme site (underlined) followed by 18 nucleotides of ICE-LAP-3 coding sequence starting from the presumed terminal amino acid of the processed protein codon

<400> 5

gatcgatcc atgcgtgcgg ggacacgggt c

31

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<210> 6
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Contains complementary sequences to an Xba I site followed by 21
nucleotides of ICE-LAP-3

<400> 6
gtactctaga tcattcaccc tggtgaggaa t 31

<210> 7
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Contains a Bam HI restriction enzyme site followed by 18
nucleotides of ICE-LAP-4 coding sequence starting from the
presumed terminal amino acid of the processed protein codon

<400> 7
gatcggatcc atggagaaca ctgaaaactc a 31

<210> 8
<211> 31
<212> DNA
<213> Artificial sequence

<220>
<223> Contains complementary sequences to an Xba I site followed by 21
nucleotides of ICE-LAP-4

<400> 8
gtactctaga ttagtgataa aaatagagtt c 31

<210> 9
<211> 22
<212> DNA
<213> Artificial sequence

<220>
<223> Contains the ICE-LAP-3 translational initiation site ATG followed
by 5 nucleotides of ICE-LAP-3 coding sequence starting from the
initiation codon

<400> 9
gactatgcgt gcggggacac gg 22

<210> 10
<211> 53
<212> DNA
<213> Artificial sequence

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<220>
<223> Contains translation stop codon, HA tag and the last 21
      nucleotides of the ICE-LAP-3 coding sequence, not including the
      stop codon

<400> 10
aatcaagcgt agtctgggac gtcgtatggg tattcacccct ggtggaggat ttg      53

<210> 11
<211> 21
<212> DNA
<213> Artificial sequence

<220>
<223> Contains the ICE-LAP-4 translational initiation site, ATG,
      followed by 15 nucleotides of ICE-LAP-4 coding sequence starting
      from the initiation codon

<400> 11
accatggaga acactgaaaaa c      21

<210> 12
<211> 53
<212> DNA
<213> Artificial sequence

<220>
<223> Contains translation stop codon, HA tag and the last 21
      nucleotides of the ICE-LAP-4 coding sequence, not including the
      stop codon

<400> 12
aatcaagcgt agtctgggac gtcgtatggg tagtgataaa aatagagttc ttt      53

<210> 13
<211> 503
<212> PRT
<213> Caenorhabditis elegans

<400> 13

Met Met Arg Gln Asp Arg Arg Ser Leu Leu Glu Arg Asn Ile Met Met
1           5           10          15

Phe Ser Ser His Leu Lys Val Asp Glu Ile Leu Glu Val Leu Ile Ala
20          25          30

Lys Gln Val Leu Asn Ser Asp Asn Gly Asp Met Ile Asn Ser Cys Gly
35          40          45

Thr Val Arg Glu Lys Arg Arg Glu Ile Val Lys Ala Val Gln Arg Arg
50          55          60

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Gly Asp Val Ala Phe Asp Ala Phe Tyr Asp Ala Leu Arg Ser Thr Gly  
65 70 75 80

His Glu Gly Leu Ala Glu Val Leu Glu Pro Leu Ala Arg Ser Val Asp  
85 90 95

Ser Asn Ala Val Glu Phe Glu Cys Pro Met Ser Pro Ala Ser His Arg  
100 105 110

Arg Ser Arg Ala Leu Ser Pro Ala Gly Tyr Thr Ser Pro Thr Arg Val  
115 120 125

His Arg Asp Ser Val Ser Ser Val Ser Ser Phe Thr Ser Tyr Gln Asp  
130 135 140

Ile Tyr Ser Arg Ala Arg Ser Arg Ser Arg Ser Arg Ala Leu His Ser  
145 150 155 160

Ser Asp Arg His Asn Tyr Ser Ser Pro Pro Val Asn Ala Phe Pro Ser  
165 170 175

Gln Pro Ser Ser Ala Asn Ser Ser Phe Thr Gly Cys Ser Ser Leu Gly  
180 185 190

Tyr Ser Ser Ser Arg Asn Arg Ser Phe Ser Lys Ala Ser Gly Pro Thr  
195 200 205

Gln Tyr Ile Phe His Glu Glu Asp Met Asn Phe Val Asp Ala Pro Thr  
210 215 220

Ile Ser Arg Val Phe Asp Glu Lys Thr Met Tyr Arg Asn Phe Ser Ser  
225 230 235 240

Pro Arg Gly Met Cys Leu Ile Ile Asn Asn Glu His Phe Glu Gln Met  
245 250 255

Pro Thr Arg Asn Gly Thr Lys Ala Asp Lys Asp Asn Leu Thr Asn Leu  
260 265 270

Phe Arg Cys Met Gly Tyr Thr Val Ile Cys Lys Asp Asn Leu Thr Gly  
275 280 285

Arg Gly Met Leu Leu Thr Ile Arg Asp Phe Ala Lys His Glu Ser His  
290 295 300

Gly Asp Ser Ala Ile Leu Val Ile Leu Ser His Gly Glu Glu Asn Val  
305 310 315 320

Ile Ile Gly Val Asp Asp Ile Pro Ile Ser Thr His Glu Ile Tyr Asp  
325 330 335

Leu Leu Asn Ala Ala Asn Ala Pro Arg Leu Ala Asn Lys Pro Lys Ile  
340 345 350

Val Phe Val Gln Ala Cys Arg Gly Glu Arg Arg Asp Asn Gly Phe Pro  
355 360 365

Val Leu Asp Ser Val Asp Gly Val Pro Ala Phe Leu Arg Arg Gly Trp  
370 375 380

Asp Asn Arg Asp Gly Pro Leu Phe Asn Phe Leu Gly Cys Val Arg Pro  
385 390 395 400

Gln Val Gln Gln Val Trp Arg Lys Lys Pro Ser Gln Ala Asp Ile Leu  
405 410 415

Ile Ala Tyr Ala Thr Thr Ala Gln Tyr Val Ser Trp Arg Asn Ser Ala  
420 425 430

Arg Gly Ser Trp Phe Ile Gln Ala Val Cys Glu Val Phe Ser Thr His  
435 440 445

Ala Lys Asp Met Asp Val Val Glu Leu Leu Thr Glu Val Asn Lys Lys  
450 455 460

Val Ala Cys Gly Phe Gln Thr Ser Gln Gly Ser Asn Ile Leu Lys Gln  
465 470 475 480

Met Pro Glu Met Thr Ser Arg Leu Leu Lys Lys Phe Tyr Phe Trp Pro  
485 490 495

Glu Ala Arg Asn Ser Ala Val  
500

<210> 14  
<211> 404  
<212> PRT  
<213> Homo sapiens

<400> 14

Met Ala Asp Lys Val Leu Lys Glu Lys Arg Lys Leu Phe Ile Arg Ser

1

5

10

15

Met Gly Glu Gly Thr Ile Asn Gly Leu Leu Asp Glu Leu Leu Gln Thr  
20 25 30

Arg Val Leu Asn Lys Glu Glu Met Glu Lys Val Lys Arg Glu Asn Ala  
35 40 45

Thr Val Met Asp Lys Thr Arg Ala Leu Ile Asp Ser Val Ile Pro Lys  
50 55 60

Gly Ala Gln Ala Cys Gln Ile Cys Ile Thr Tyr Ile Cys Glu Glu Asp  
65 70 75 80

Ser Tyr Leu Ala Gly Thr Leu Gly Leu Ser Ala Asp Gln Thr Ser Gly  
85 90 95

Asn Tyr Leu Asn Met Gln Asp Ser Gln Gly Val Leu Ser Ser Phe Pro  
100 105 110

Ala Pro Gln Ala Val Gln Asp Asn Pro Ala Met Pro Thr Ser Ser Gly  
115 120 125

Ser Glu Gly Asn Val Lys Leu Cys Ser Leu Glu Glu Ala Gln Arg Ile  
130 135 140

Trp Lys Gln Lys Ser Ala Glu Ile Tyr Pro Ile Met Asp Lys Ser Ser  
145 150 155 160

Arg Thr Arg Leu Ala Leu Ile Ile Cys Asn Glu Glu Phe Asp Ser Ile  
165 170 175

Pro Arg Arg Thr Gly Ala Glu Val Asp Ile Thr Gly Met Thr Met Leu  
180 185 190

Leu Gln Asn Leu Gly Tyr Ser Val Asp Val Lys Lys Asn Leu Thr Ala  
195 200 205

Ser Asp Met Thr Thr Glu Leu Glu Ala Phe Ala His Arg Pro Glu His  
210 215 220

Lys Thr Ser Asp Ser Thr Phe Leu Val Phe Met Ser His Gly Ile Arg  
225 230 235 240

Glu Gly Ile Cys Gly Lys Lys His Ser Glu Gln Val Pro Asp Ile Leu

245

250

255

Gln Leu Asn Ala Ile Phe Asn Met Leu Asn Thr Lys Asn Cys Pro Ser  
260 265 270

Leu Lys Asp Lys Pro Lys Val Ile Ile Ile Gln Ala Cys Arg Gly Asp  
275 280 285

Ser Pro Gly Val Val Trp Phe Lys Asp Ser Val Gly Val Ser Gly Asn  
290 295 300

Leu Ser Leu Pro Thr Thr Glu Glu Phe Glu Asp Asp Ala Ile Lys Lys  
305 310 315 320

Ala His Ile Glu Lys Asp Phe Ile Ala Phe Cys Ser Ser Thr Pro Asp  
325 330 335

Asn Val Ser Trp Arg His Pro Thr Met Gly Ser Val Phe Ile Gly Arg  
340 345 350

Leu Ile Glu His Met Gln Glu Tyr Ala Cys Ser Cys Asp Val Glu Glu  
355 360 365

Ile Phe Arg Lys Val Arg Phe Ser Phe Glu Gln Pro Asp Gly Arg Ala  
370 375 380

Gln Met Pro Thr Thr Glu Arg Val Thr Leu Thr Arg Cys Phe Tyr Leu  
385 390 395 400

Phe Pro Gly His